

In the claims:

Amend claims 28-30 as follows and add new claims 59-60.

C 28. (Currently Amended) A cytotoxic T-cell epitope having an amino acid sequence ILVPKVSGL (SEQ ID NO: 1), RLVWACVGV (SEQ ID NO: 2), HLFNRAGTV (SEQ ID NO: 3), YLRREQMFV (SEQ ID NO: 4), TLQANKSEV (SEQ ID NO: 5), ILEDWNFGL (SEQ ID NO: 6), SLWLPSEATVYL (SEQ ID NO: 7), NLASSNYFPT (SEQ ID NO: 8), TLTADVMTYI (SEQ ID NO: 9), YLPPVPVSKV (SEQ ID NO: 10), YDLQFIFQL (SEQ ID NO: 11), ICWGNQLFV (SEQ ID NO: 12), FYNPDTQRL (SEQ ID NO: 13), and/or a functionally active variant thereof.

29. (Currently Amended) The cytotoxic T-cell epitope as claimed in claim 28, wherein said variant has a sequence homology to ILVPKVSGL (SEQ ID NO: 1), RLVWACVGV (SEQ ID NO: 2), HLFNRAGTV (SEQ ID NO: 3), YLRREQMFV (SEQ ID NO: 4), TLQANKSEV (SEQ ID NO: 5), ILEDWNFGL (SEQ ID NO: 6), SLWLPSEATVYL (SEQ ID NO: 7), NLASSNYFPT (SEQ ID NO: 8), TLTADVMTYI (SEQ ID NO: 9), YLPPVPVSKV (SEQ ID NO: 10), YDLQFIFQL (SEQ ID NO: 11), ICWGNQLFV (SEQ ID NO: 12), FYNPDTQRL (SEQ ID NO: 13), of at least approx. 65%, preferably at least approx. 75% and in particular at least approx. 85% at the amino acid level.

30. (Currently Amended) The cytotoxic T-cell epitope as claimed in claim 28, wherein said variant is structurally homologous to ILVPKVSGL (SEQ ID NO: 1), RLVWACVGV (SEQ ID NO: 2), HLFNRAGTV (SEQ ID NO: 3), YLRREQMFV (SEQ ID NO: 4), TLQANKSEV (SEQ ID NO: 5), ILEDWNFGL (SEQ ID NO: 6), SLWLPSEATVYL (SEQ ID NO: 7), NLASSNYFPT (SEQ ID NO: 8), TLTADVMTYI (SEQ ID NO: 9), YLPPVPVSKV (SEQ ID NO: 10), YDLQFIFQL (SEQ ID NO: 11), ICWGNQLFV (SEQ ID NO: 12), or FYNPDTQRL (SEQ ID NO: 13).

59. (New) The compound as claimed in claim 32, wherein said variant has a sequence homology to ILVPKVSGL (SEQ ID NO: 1), RLVWACVGV (SEQ ID NO: 2), HLFNRAGTV (SEQ ID NO: 3), YLRREQMFV (SEQ ID NO: 4), TLQANKSEV (SEQ ID NO: 5), ILEDWNFGL (SEQ ID NO: 6), SLWLPSEATVYL (SEQ ID NO: 7), NLASSNYFPT (SEQ ID NO: 8), TLTADVMTYI (SEQ ID NO: 9), YLPPVPVSKV (SEQ ID NO: 10), YDLQFIFQL (SEQ ID NO: 11), ICWGNQLFV (SEQ ID NO: 12), FYNPDTQRL (SEQ ID NO: 13), of at least approx. 65%, preferably at least approx. 75% and in particular at least approx. 85% at the amino acid level.

60. (New) The compound as claimed in claim 32, wherein said variant is structurally homologous to ILVPKVSGL (SEQ ID NO: 1), RLVWACVGV (SEQ ID NO: 2), HLFNRAGTV (SEQ ID NO: 3), YLRREQMFV (SEQ ID NO: 4), TLQANKSEV

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(SEQ ID NO: 5), ILEDWNFGL (SEQ ID NO: 6), SLWLPSEATVYL (SEQ ID NO: 7),
NLASSNYFPT (SEQ ID NO: 8), TLTADVMTYI (SEQ ID NO: 9), YLPPVPVSKV
(SEQ ID NO: 10), YDLQFIFQL (SEQ ID NO: 11), ICWGNQLFV (SEQ ID NO: 12), or
FYNPDTQRL (SEQ ID NO: 13).
